

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/757,049A

DATE: 10/26/2001

TIME: 13:11:47

Input Set : A:\#552399v2.asc

Output Set: N:\CRF3\10262001\I757049A.raw

Does Not Comply
Corrected Diskette Needed

W--> 1 16

4 <110> APPLICANT: BERNSTEIN, Harold S.

5 COUGHLIN, Shaun R.

7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE

8 PROGRESSION

10 <130> FILE REFERENCE: UCSF-020/02US

C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/757,049A

13 <141> CURRENT FILING DATE: 2001-01-08

15 <150> PRIOR APPLICATION NUMBER: US 09/156,316

16 <151> PRIOR FILING DATE: 1998-09-18

18 <150> PRIOR APPLICATION NUMBER: US 60/060,688

19 <151> PRIOR FILING DATE: 1997-09-22

21 <160> NUMBER OF SEQ ID NOS: 50

23 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

401 <210> SEQ ID NO: 11

402 <211> LENGTH: 2837

403 <212> TYPE: DNA

404 <213> ORGANISM: Homo sapiens

406 <400> SEQUENCE: 11

E--> 407 ggcagcagag gaagtggcgg ctttgagtcc ggtggcccaa tcgctgttac tacttctctg → 60

408 60

E--> 409 aagctcctct cggtgcttg ccgagacacc ctgccgcaa gatgcctcga attatgatca → 120

410 120

E--> 411 aggggggagcgt atggaggaat accgaggatg aaattctgaa agcagcggta atgaaatag

412 180

E--> 413 ggaaaaatca gtggtctagg attgcctcat tgctgcatag aaaatcagca aagcagtgc

414 240

E--> 415 aagccagatg gtatgaatgg ctggatccaa gcattaagaa gacagaatgg tccagagaag

416 300

E--> 417 aagaggaaaa actcttgac ttggccaagt tgatgccaac tcagtggagg accattgctc

418 360

E--> 419 caatcattgg aagaacagcg gcccagtgtc tagaacacta tgaatttctt ctggataaag

420 420

E--> 421 ctgcccaaaag agacaatgaa gaggaacaa cagatgatcc acgaaaactt aaacctggag

422 480

E--> 423 aaatagatcc aaatccagaa acaaaaccag cgcggcctga tccaattgat atggatgagg

424 540

E--> 425 atgaacttga gatgctttct gaagccagag cccgcttggc taatactcag ggaaagaagg

426 600

E--> 427 ccaagaggaa agcaagagag aaacaattgg aagaagcaag acgtcttgct gccctccaaa

428 660

E--> 429 aaagaagaga acttcgagca gctggcatag aaattcagaa gaaaagaaaa aggaagagag

430 720

format error

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```

E--> 431 gagttgatta taatgccgaa atcccatttg aaaaaaagcc tgcccttgggt ttttatgata
      432 780
E--> 433 cttctgagga aaactaccaa gctcttgacg cagatttcag gaaattaaga caacaggatc
      434 840
E--> 435 ttgatgggga gctaagatct gaaaaagaag gaagagatag aaaaaaagac aaacagcatt
      436 900
E--> 437 tgaaaaggaa aaaagaatct gattttaccat cagctattct tcaaactagt ggtgtttctg
      438 960
E--> 439 aatttactaa aaagagaagc aaactagtac ttcttgcccc tcagatttca gatgcagaac
      440 1020
E--> 441 tccaggaagt tgtaaaagta ggccaagcga gtgaaattgc acgtcaaact gccgaggaat
      442 1080
E--> 443 ctggcataac aaattctgct tccagtacac ttttgtctga gtacaatgtc accaacaaca
      444 1140
E--> 445 gcgttgctct tagaacacca cgaacaccag ctcccagga cagaattctg caggaagccc
      446 1200
E--> 447 agaacctcat ggccctcacc aatgtggaca ccccatgaa aggtggactt aatacccat
      448 1260
E--> 449 tgcattgagag tgactttctca ggtgtaactc cacagcgaca agttgtacag actccaaaca
      450 1320
E--> 451 cagttctctc tactccattc aggactcctt ctaatggagc tgaagggctg actccccgga
      452 1380
E--> 453 gtggaacaac tcccaaacca gttattaaact ctactccggg tagaactcct ctctgagaca
      454 1440
E--> 455 agttaaacat taatcccagag gatggaatgg cagactatag tgatccctct tacgtgaagc
      456 1500
E--> 457 agatggaaag agaatcccga gaacatctcc gtttaggggtt gttgggcctt cctgccccta
      458 1560
E--> 459 agaattgatt tgaaattggt ctaccagaaa atgccgagaa ggagctggaa gaacgtgaaa
      460 1620
E--> 461 tagatgatac ttacattgaa gatgctgctg atgtggatgc tcgaaagcag gccatacgag
      462 1680
E--> 463 atgcagagcg tgtaaaggaa atgaaacgaa tgcataaagc tgtccagaaa gatctgccaa
      464 1740
E--> 465 gaccatcaga agtaaataaa actattctaa gacccttaaa tgtagaaccg cctttaacag
      466 1800
E--> 467 atttacagaa aagtgaagaa ctaatacaaaa aagaaatgat cacaatgctt cattatgacc
      468 1860
E--> 469 ttctacatca cccttatgaa ccatctggaa ataaaaaagg caaaactgta gggtttggtg
      470 1920
E--> 471 ccaataattc agagcacatt acctatctgg aacataatcc ttatgaaaag ttctccaaag
      472 1980
E--> 473 aagagctgaa aaaggcccag gatgttttgg tgcaggagat ggaagtgggt aaacaaggaa
      474 2040
E--> 475 tgagccatgg agagctctca agtgaagctt ataaccaggt gtgggaagaa tgctacagtc
      476 2100
E--> 477 aagttttata tcttctggg cagagccgct acacacgggc caatctggct agtaaaaagg
      478 2160
E--> 479 acagaattga atcacttgaa aagaggctcg agataaacag gggtcacatg acgacagaag

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same

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```

480 2220
E--> 481 ccaagagggc tgcaaagatg gaaaagaaga tgaaaatttt gcttgggggt taccagtctc
482 2280
E--> 483 gtgctatggg gctcatgaaa cagttgaatg acttatggga ccaaattgaa caggctcact
484 2340
E--> 485 tggagttacg cacttttgaa gaactcaaga aacatgaaga ttctgctatt ccccgagggc
486 2400
E--> 487 tagagtgtct aaaagaagac gttcagcgac aacaagaaag agaaaaggaa cttcaacata
488 2460
E--> 489 gatatgctga tttgctgctg gagaaagaga ctttaaagtc aaaatttctga agtacagttt
490 2520
E--> 491 atattctgtc acaggattaa ttaattgccg gttttcatac tctagaaggc tgaaactgat
492 2580
E--> 493 gtttatcttc attgacaaat ttaccacca tctgtgggtt ttcagttgtt tatttttaaat
494 2640
E--> 495 gatatcgatc ttacacattc tgtgtataaaa gaccttaact ccacaggacg gacattttag
496 2700
E--> 497 agttttaaatt attaaggcta tcattctttt agtaatgtca tatttgcaaa ctttttttagt
498 2760
E--> 499 tttggccttt aatttaaaaa gcctaatttt aaagtgtgc ctgtgagtaa ctcttgaata
500 2820
E--> 501 aaaacaaaaat ataaaaa
502 2837
517 <210> SEQ ID NO: 13
518 <211> LENGTH: 12
519 <212> TYPE: DNA
520 <213> ORGANISM: Artificial Sequence
522 <220> FEATURE:
523 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
525 <400> SEQUENCE: 13
E--> 526 gatttaacat aa
527 12
529 <210> SEQ ID NO: 14
530 <211> LENGTH: 9
531 <212> TYPE: DNA
532 <213> ORGANISM: Artificial Sequence
534 <220> FEATURE:
535 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
537 <400> SEQUENCE: 14
E--> 538 ttaacataa
539 9
541 <210> SEQ ID NO: 15
542 <211> LENGTH: 15
543 <212> TYPE: DNA
544 <213> ORGANISM: Homo sapiens
546 <400> SEQUENCE: 15
E--> 547 aataaaatca aaatt
548 15
550 <210> SEQ ID NO: 16

```

Done

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Input Set : A:\#552399v2.asc

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```

551 <211> LENGTH: 15
552 <212> TYPE: DNA
553 <213> ORGANISM: Homo sapiens
555 <400> SEQUENCE: 16
E--> 556 aaaggggaac                                acttt
557 15
559 <210> SEQ ID NO: 17
560 <211> LENGTH: 55
561 <212> TYPE: DNA
562 <213> ORGANISM: Artificial Sequence
564 <220> FEATURE:
565 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
567 <220> FEATURE:
W--> 568 <221> NAME/KEY: misc difference
569 <222> LOCATION: (21)..(35)
570 <223> OTHER INFORMATION: n = Any Nucleotide
572 <400> SEQUENCE: 17
E--> 573 cgctcgaggg atccgaattc nnnnnnnnnn nnnnntctag aaagcttgtc gacgc
574 55
576 <210> SEQ ID NO: 18
577 <211> LENGTH: 20
578 <212> TYPE: DNA
579 <213> ORGANISM: Artificial Sequence
581 <220> FEATURE:
582 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
584 <400> SEQUENCE: 18
E--> 585 gcgtcgacaa                                gctttctaga
586 20
588 <210> SEQ ID NO: 19
589 <211> LENGTH: 20
590 <212> TYPE: DNA
591 <213> ORGANISM: Artificial Sequence
593 <220> FEATURE:
594 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
596 <400> SEQUENCE: 19
E--> 597 cgctcgaggg                                atccgaattc
598 20
600 <210> SEQ ID NO: 20
601 <211> LENGTH: 11
602 <212> TYPE: DNA
603 <213> ORGANISM: Artificial Sequence
605 <220> FEATURE:
606 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
608 <400> SEQUENCE: 20
E--> 609 atttaacata                                a
610 11
612 <210> SEQ ID NO: 21
613 <211> LENGTH: 12
614 <212> TYPE: DNA

```

same

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Input Set : A:\#552399v2.asc

Output Set: N:\CRF3\10262001\I757049A.raw

615 <213> ORGANISM: Artificial Sequence
617 <220> FEATURE:
618 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
620 <400> SEQUENCE: 21
E--> 621 tatttaacat aa
622 12
624 <210> SEQ ID NO: 22
625 <211> LENGTH: 12
626 <212> TYPE: DNA
627 <213> ORGANISM: Artificial Sequence
629 <220> FEATURE:
630 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
632 <400> SEQUENCE: 22
E--> 633 gctttaacat as
634 12
636 <210> SEQ ID NO: 23
637 <211> LENGTH: 12
638 <212> TYPE: DNA
639 <213> ORGANISM: Artificial Sequence
641 <220> FEATURE:
642 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
644 <400> SEQUENCE: 23
E--> 645 gagttaacat aa
646 12
648 <210> SEQ ID NO: 24
649 <211> LENGTH: 12
650 <212> TYPE: DNA
651 <213> ORGANISM: Artificial Sequence
653 <220> FEATURE:
654 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
656 <400> SEQUENCE: 24
E--> 657 gatgtaacat aa
658 12
660 <210> SEQ ID NO: 25
661 <211> LENGTH: 12
662 <212> TYPE: DNA
663 <213> ORGANISM: Artificial Sequence
665 <220> FEATURE:
666 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
668 <400> SEQUENCE: 25
E--> 669 gattgaacat aa
670 12
672 <210> SEQ ID NO: 26
673 <211> LENGTH: 12
674 <212> TYPE: DNA
675 <213> ORGANISM: Artificial Sequence
677 <220> FEATURE:
678 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
680 <400> SEQUENCE: 26

same

RAW SEQUENCE LISTING

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TIME: 13:11:47

Input Set : A:\#552399v2.asc

Output Set: N:\CRF3\10262001\I757049A.raw

E--> 681 gatttcacat aa
682 12
684 <210> SEQ ID NO: 27
685 <211> LENGTH: 12
686 <212> TYPE: DNA
687 <213> ORGANISM: Artificial Sequence
689 <220> FEATURE:
690 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
692 <400> SEQUENCE: 27

E--> 693 gatttaccat aa
694 12
696 <210> SEQ ID NO: 28
697 <211> LENGTH: 12
698 <212> TYPE: DNA
699 <213> ORGANISM: Artificial Sequence
701 <220> FEATURE:
702 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
704 <400> SEQUENCE: 28

E--> 705 gatttaatat aa
706 12
708 <210> SEQ ID NO: 29
709 <211> LENGTH: 12
710 <212> TYPE: DNA
711 <213> ORGANISM: Artificial Sequence
713 <220> FEATURE:
714 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
716 <400> SEQUENCE: 29

E--> 717 gatttaacct aa
718 12
720 <210> SEQ ID NO: 30
721 <211> LENGTH: 12
722 <212> TYPE: DNA
723 <213> ORGANISM: Artificial Sequence
725 <220> FEATURE:
726 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
728 <400> SEQUENCE: 30

E--> 729 gatttaacag aa
730 12
732 <210> SEQ ID NO: 31
733 <211> LENGTH: 12
734 <212> TYPE: DNA
735 <213> ORGANISM: Artificial Sequence
737 <220> FEATURE:
738 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
740 <400> SEQUENCE: 31

E--> 741 gatttaacat ca
742 12

same

VERIFICATION SUMMARY

DATE: 10/26/2001

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TIME: 13:11:48

Input Set : A:\#552399v2.asc

Output Set: N:\CRF3\10262001\I757049A.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:407 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:11
M:254 Repeated in SeqNo=11
L:526 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:13
L:538 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:9 SEQ:14
L:547 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:15
L:556 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:16
L:568 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:573 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:17
L:585 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:18
L:597 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:19
L:609 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:11 SEQ:20
L:621 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:21
L:633 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:22
L:645 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:23
L:657 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:24
L:669 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:25
L:681 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:26
L:693 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:27
L:705 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:28
L:717 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:29
L:729 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:30
L:741 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:31
L:753 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:32
L:762 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:33
L:771 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:34
L:780 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:35
L:792 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:36
L:804 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:37
L:817 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:38
L:829 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:39
L:841 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:40
L:853 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:41
L:865 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:42
L:877 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:43
L:889 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:44
L:901 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:45
L:913 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:46
M:254 Repeated in SeqNo=46
L:927 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:47
L:939 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:48
M:254 Repeated in SeqNo=48
L:953 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:49
L:965 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:12 SEQ:50